

 (TM)

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MPSch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 13 09:28:01 2000; MasPar time 17.23 Seconds

Tabular output not generated.

Title: >JUS-08-978-217-15

Description: (1-371) from US08978217.pep

Perfect Score: 2706

Sequence: 1 MAATCEISINVFSNYFNMYS.....YKFGKNSSGKKEEEVGESRN 371

Scoring table: PAM 150

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% summaries
 Database: Listing first 45 summaries

pir60
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES
 %
 Result No. Score Query Match Length DB ID Description Pred. No.

RESULT	1	ENTRY	JW048	#type complete
TITLE		ORGANISM	ets	transcription factor - mouse
DATE		ACCESSIONS	#formal_name Mus musculus	#common_name house mouse
SEARCHED:	10-Jul-1998	ACCESSIONS	JW048	#sequence_revision 10-Jul-1998 #text_change
SEARCHED:	17-Mar-1999	REFERENCE	JW048	
SEARCHED:		#authors	Bocchert, M.A.; Kleinbaum, L.A.; Sun, L.Y.; Burton, F.H.	
SEARCHED:		#journal	Biochem. Biophys. Res. Commun. (1998) 246:176-181	
SEARCHED:		#title	Puff 74E protein, a new member of the molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family.	
SEARCHED:		#cross-references	MUID:98262938	
SEARCHED:		#accession	JW048	
SEARCHED:		#molecule_type	mRNA	
SEARCHED:		#residues	1-300	#label BOC
SEARCHED:		CLASSIFICATION	1-300 #label ets	DNA-binding domain homology
SEARCHED:		FEATURE	1-300 #label ets	DNA-binding domain homology
SEARCHED:	209-289	SUMMARY	#length 300	#domain ets DNA-binding domain homology
SEARCHED:		QUERY	24.7%; Score 668; DB 2; Length 300;	
SEARCHED:		Match	Best Local Similarity 80.8%; Pred. No. 6.68e-110;	
SEARCHED:		DB	Matches 80; Conservative 12; Mismatches 7; Indels 0; Gaps 0;	
SEARCHED:		ENTRY	Db 201 KHNPRGTHWEFIRDILSPDKNPLIKWEDRREGIFPLKRSVAOLWGKKNNSSMTY 260	
SEARCHED:		TITLE: :	

24	311	11.5	385	1	\$29844	transforming protein
25	310	11.5	462	1	\$35534	adenovirus E1A enhancer
26	310	11.5	555	1	\$24061	transcription factor
27	305	11.3	173	2	\$56646	PE-1 protein - human
28	306	11.3	250	2	\$45308	transformation protein
29	307	11.3	452	1	\$137565	transformation protein
30	307	11.3	452	1	\$17403	transformation protein
31	305	11.3	486	1	\$17403	transformation protein
32	306	11.3	548	2	\$59133	ETS2 repressor factor
33	306	11.3	732	2	\$43315	ETS domain protein ya
34	306	11.3	751	2	\$46193	88K B-26-specific domain protein
35	304	11.2	272	2	\$454617	transcription factor
36	304	11.2	453	1	\$49013	transforming protein
37	304	11.2	478	1	\$60754	transcription factor
38	297	11.0	477	1	\$46396	transcription factor
39	297	11.0	138893	1	\$138893	transcription factor
40	298	11.0	510	1	\$43692	transcription factor
41	294	10.9	342	2	\$46396	etr-related protein 7
42	294	10.9	472	1	\$53236	transcription factor
43	273	10.1	472	1	\$53236	transcription factor
44	274	10.1	479	1	\$11224	transcription factor
45	274	10.0	268	2	\$11224	transcription factor

ALIGNMENTS

GENETICS
#gene FlyBase:Eip74EF
#cross-references FlyBase:FBgn0000567
#map-position 3' 74EF
CLASSIFICATION #superfamily ets DNA-binding domain homology
KEYWORDS alternative splicing; DNA binding; transcription regulation
FEATURE #length 883 #molecular-weight 94819 #checksum 1974
SUMMARY

Query Match 13.7%; Score 372; DB 2; Length 883;
Best Local Similarity 34.9%; Pred. No. 9.06e-49; Indels 46; Mismatches 57; Gaps 7;
Matches 59; Conservative 46; Mismatches 57; Indels 7; Gaps 7;

Db 707 SSSSSAAVAAMLSASAAATAAAGGSQSVIOPATSSY-S-YDLS-YMLELGGFQOR 763
OY 186 PGASPGSSPDVSTARTATPQSSHASGSSPDVLDLTERSKVPRPDDFTYKKGPKHGR 245
Db 764 KAKKPKR-PK-L-E-MGVKRSRSRGSTTYLWEFLIKLQDREYCPRFIKWTNRERGVFKL 819
OY 246 KRGPRPKLSKEYWDCLEGKKSKHAPRGTHIWEFIRDILHPELNNEGIMKWENRHEGVFKF 305
Db 820 VDSKAVSRWLGGMHNKPDMVYETMGRALRYYQORGILAKUDQGQLVHF 868
OY 306 LRSEAVAOLWGMOKKKNSNMNTYKLSRAMYYKREILERVDGRRLVYF 354

RESULT 6 B53225 #type complete
ENTRY edysone-induced protein E74A - fruit fly (Drosophila
TITLE virilis)
ORGANISM #formal_name Drosophila virilis
DATE 12-May-1994 #sequence_revision 12-May-1994 #text_change
ACCESSIONS B53225
#authors Jones, C.W.; Dalton, M.W.; Townley, L.H.
#title Inter-specific comparisons of the structure and regulation of
#cross-references MUID:91206627 the Drosophila edysone-inducible gene E74.
#accession B53225 preliminary; not compared with conceptual translation
#status #molecule_type mRNA
#residues 1-873 #label JON
##CROSS-references GB:X59493

GENETICS
#gene FlyBase:Dv17Eip4EF
#cross-references FlyBase:FBgn0013076
CLASSIFICATION #superfamily ets DNA-binding domain homology
FEATURE #length 873 #molecular-weight 94630 #checksum 6269
SUMMARY

Query Match 13.6%; Score 369; DB 2; Length 873;
Best Local Similarity 47.3%; Pred. No. 3.58e-48; Indels 43; Conservative 20; Mismatches 28; Indels 0; Gaps 0; Matches 43; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Db 768 KRSREGSTYTLWEFLIKLQDREYCPRFIKWTNRERGVFKLVSKAVERLWGMHKNKPD 827
OY 264 KKSCHKAPRGTHLWEFIRDILHPELNNEGIMKWENRHEGVFKLSEAVAOLWGMOKKKNS 323
Db 828 MNVYEMGRALRYYQORGILAKUDQGQLVHF 858
OY 324 MTYERKLSRAMYYKREILERVDGRRLVYF 354

RESULT 8 A43361 #type complete
ENTRY Ets related transcription factor Elf-1 - human
TITLE E4-like factor Elf-1
ACCESSIONS A43361; A42122
REFERENCE A43361
#authors Leiden, J.M.; Wang, C.Y.; Petryniak, B.; Markovitz, D.M.; Nabel, G.J.; Thompson, C.B.
#journal J. Virol. (1992) 66:5990-5997
#title A novel Ets-related transcription factor, Elf-1, binds to human immunodeficiency virus type 2 regulatory elements that are required for inducible trans activation in T cells.
#accession A43361
#molecule_type mRNA
#residues 1-619 #label LEI
##CROSS-references GB:MB8822

REFERENCE A42122
#authors Thompson, C.B.; Wang, C.Y.; Ho, I.C.; Bohjanen, P.R.; Markovitz, D.M.; Nabel, G.J.; Petryniak, B.; June, C.H.; Miesfeld, S.; Zhang, L.; Leiden, J.M.
#journal Mol. Cell. Biol. (1992) 12:1043-1053
#title cis-acting sequences required for inducible interleukin-2 enhancer function bind a novel Ets-related protein, Elf-1.
#cross-references MUID:92186836

##status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 204-282
#experimental_source T-cells
##note sequence extracted from NCBI backbone (NCBIP:88288)

GENETICS
#gene GDB:Elf1
#cross-references GDB:131648
#map-position 1p36-p36
CLASSIFICATION #superfamily ets DNA-binding domain homology
KEYWORDS DNA binding; transcription regulation
FEATURE 210-290
SUMMARY #length 619 #molecular-weight 67455 #checksum 5026

RESULT 7 G02318 #type complete
ENTRY Ets transcription factor - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
DATE 17-Jul-1998

